

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

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ATC TTTGTTCA GT TTACCTCAGG GCTATTATGA 33

34 AATGAAATGA GATAACCAAT GTGAAAGTCC TATAAACTGT ATAGCCTCCA TTGGATGTA 93

94 TGTCTTGGC AGGATGATAA AGAACAGGA AGAAGGAGTA TCCACGTTAG CCAAGTGTCC 153

154 AGGCTGTGTC TGCTCTTATT TTGAGTGCAG ATGTTGCTCC TGACAGAAGC TATTCTTCAG 213

214 GAAACATCAC ATCCAATATG GTAAATCCAT CAAACAGGAG CTAAGAAACA GGAATGAGAT 273

274 GGGCACTTGC CCAAGGAAAA ATGCCAGGAG AGCAAATAAT GATGAAAAAT AAACCTTTCC 333

334 CTTTGTCCCC AATTCAGGA AAAATGATG AGGACCAAAA TCAATGAATA AGGAAAACAG 393  
(Pr1.FPIII) CCTG AAAATGAATA AGAAA

394 CTCAGAAAAA AGATGTTTCC AAATGGTAA TTAAGTATT TTGTCCTGGG AAGAGACCTC 453  
(PR/GR-MMTV) T GTTCTTTGG AA  
(SSRE) GAGACC

454 CATGTGAGCT TGATGGAAA ATGGGAAAAA CGTCAAAGC ATGATCTGAT CAGATCCCA 513

514 AGTGGATTAT TATTTTAAAA ACCAGATGGC ATCACTCTGG GGAGGCAAGT TCAGGAAGGT 573

574 CATGTTAGCA AAGGACATAA CAATAACAGC AAAATCAAAA TTCCGCAAAT GCAGGAGGAA 633  
CCTTTAG-A AAGGACAAAA CAGAATG (nGRE-PRL)

634 AATGGGGACT GGGAAAGCTT TCATAACAGT GATTAGGCAG TTGACCATGT TCGAACACC 693

694 TCCCCGTCTA TACCAAGGAA CACAAAATT GACTGGCTA AGCCTGGACT TTCAAGGGAA 753  
GCCTGGACT GTC (CBE-P53)

754 ATATGAAAAA CTGAGAGCAA AACAAAAGAC ATGGTTAAAA GGCAACCAGA ACATTGTGAG 813  
ATTTTCTGA TTGGTTAAAA GT (NFE1)

814 CCTTCAAAGC AGCAGTGCCTT CTCAGCAGGG ACCCTGAGGC ATTTGCCTTT AGGAAGGCCA 873  
G ACCCTGAGGC T (KTF.1-CS)

874 GTTTCTTAA GGAATCTTAA GAAACTCTTG AAAGATCATG AATTTAACCC ATTTTAAGTA 933

934 TAAAACAAAT ATGCGATGCA TAATCAGTTT AGACATGGT CCCAATTTTA TAAAGTCAGG 993  
(PRE-lysozyme) AGGCCGT

994 CATAACAAGGA TAACGTGTCC CAGCTCCGGA TAGGTCAGAA ATCATTAGAA ATCACTGTGT 1053  
GATCCAAGGA GCAGAAGTTC CAGCTATGGT CAG (GRE-hMT) GG TACACTGTGT

1054 CCCCATCCTA ACTTTTCAG AATGATCTGT CATAGCCCTC ACACACAGGC CCGATGTGTC 1113  
CCT

1114 TGACCTACAA CCACATCTAC AACCCAAGTG CCTCAACCCT TGTAAACGTG TCATCTCA 1173

FIG.1A

APPROVED	O.G. FIG.	
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FIG. 1B

APPROVED	O.G. FIG.	
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2494 ATTCCAGGAG GTGGGGACTG CAGGGAGTGG GGACGCTGGG GCTGAGCGGG TGCTGAAAGG 2553  
CTGG GGAGCCTGGG GA (AP.2-SV40)

2554 CAGGAAGGTG AAAAGGGCAA GGCTGAAGCT GCCCAGATGT TCAGTGTGTT TCACGGGGCT 2613

2614 GGGAGTTTC CGTTGCTTCC TGTGAGCCTT TTTATCTTT CTCTGCTTGG AGGAGAAGAA 2673  
CT CGTTGCTTCG AG (HSTF-hsp70)

2674 GTCTATTC A TGAAGGGATG CAGTTCAT AAGTCAGCTG TTAAAATTCC AGGGTGTGCA 2733  
A

2734 TGGGTTTCC TTCACGAAGG CCTTTATTTA ATGGGAATAT AGGAAGCGAG CTCATTCCT 2793  
TGGGTTTTG (SBF.yeast)

2794 AGGCCGTTAA TTCACGGAAG AAGTGACTGG AGTCTTTCT TTCAATGTCTT CTGGGCAACT 2853

2854 ACTCAGCCCT GTGGTGGACT TGGCTTATGC AAGACGGTCG AAAACCTTGG AATCAGGAGA 2913

2914 CTCGGTTTC TTTCTGGTT TCGCCATTGGT TGGCTGTGCG ACCGTGGGCA AGTGTCTCTC 2973  
C TTTCTGGTT TGCA (NF.1-bithorax)  
(NF-MHCII/CCATTGGT T)

2974 CTTCCCTGGG CCATAGTCCTT CTCTGCTATA AAGACCCCTG CAGCTCTCGT GTTCTGTGAA 3033

3034 CACTTCCCTG TGATTCTCTG TGAGGGGGGA TGTTGAGAGG GGAAGGAGGC AGAGCTGGAG 3093

3094 CAGCTGAGCC ACAGGGGAGG TGGAGGGGGGA CAGGAAGGCA GGCAGAAGCT GGGTGCTCCA 3153

3154 TCAGTCCTCA CTGATCACGT CAGACTCCAG GACCGAGAGC CACAATGCTT CAGGAAAGCT 2943

2944 CAATGAACCC AACAGCCACA TTTCCCTTCC CTAAGCATAG ACAATGGCAT TTGCCAATAA 3273

3274 CCAAAAAGAA TGCAGAGACT AACTGGTGGT AGCTTTGCC TGGCATTCAA AACTGGGCC 3333  
GAAGTGAAT AACTG (PEA.1-Polyoma)

3334 AGAGCAAGTG GAAAATGCCA GAGATTGTTA AACTTTCAC CCTGACCAGC ACCCCACGCA 3393

3394 GCTCAGCAGT GACTGCTGAC AGCACGGAGT GACCTGCAGC GCAGGGGAGG AGAAGAAAAA 3453  
C AGGTAGAGT GACCTG (ERE.2-Vitel.)

3454 GAGAGGGATA GTGTATGAGC AAGAAAGACA GATTCTTCA AGGGCAGTGG GAATTGACCA 3513

3514 CAGGGATTAT AGTCCACGTG ATCCTGGGTT CTAGGAGGCA GGGCTATATT GTGGGGGGAA 3573  
(GRE-FLV) CGGGATAC CGAGAGAACAA GGGCTATAGG

3574 AAAATCAGTT CAAGGGAAAGT CGGGAGACCT GATTCTAAT ACTATATTTT TCCTTACAA 3633  
GAGACC (SSRE)

3634 GCTGAGTAAT TCTGAGCAAG TCACAAGGT A GTAACTGAGG CTGTAAGATT ACTTAGTTTC 3693  
(ICS-MTII/ HLA-DR/ )AGTTTC

3694 TCCTTATTAG GAACTCTTT TCTCTGTGGA GTTAGCAGCA CAAGGGCAAT CCCGTTCTT 3753  
TCCTCT

3754 TTAACAGGAA GAAAACATTC CTAAGAGTAA AGCCAAACAG ATTCAAGCCT AGGTCTTGCT 3813

3814 GACTATATGA TTGGTTTTT GAAAATCAT TTCAGCGATG TTTACTATCT GATTCAAGAAA 3873

FIG.1C

APPROVED	O.G. FIG.	
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3874 ATGAGACTAG TACCCCTTGG TCAGCTGTAA ACAAACACCC ATTTGAAAT GTCTCAAGTT 3933  
GG TCA (1/2 ERE)

3934 CAGGCTTAAC TGCAGAACCA ATCAAATAAG AATAGAATCT TTAGAGCAA CTGTGTTCT 3993

3994 CCACTCTGGA GGTGAGTCTG CCAGGGCAGT TTGGAAATAT TTACTTCACA AGTATTGACA 4053

4054 CTGTTGTTGG TATTAACAAAC ATAAAGTTGC TCAAAGGCAA TCATTATTC AAGTGGCTTA 4113

4114 AAGTTACTTC TGACAGTTT GGTATATTAA TTGGCTATTG CCATTTGCTT TTTGTTTTT 4173  
(NF.1-HCMV) TTGGCTATTG GCCA CTTT

4174 CTCTTGGGT TTATTAATGT AAAGCAGGGA TTATTAACCT ACAGTCCAGA AAGCCTGTGA 4233  
CTCTT (ISGF2)

4234 ATTTGAATGA GGAAAAAATT ACATTTTGT TTTTACCACC TTCTAACTAA ATTTAACATT 4293  
(Zn binding)-----

4294 TTATTCCATT GCGAATAGAG CCATAAACTC AAAGTGGTAA TAACAGTACC TGTGATTTG 4353

4354 TCATTACCAA TAGAAATCAC AGACATTTA TACTATATTAA CAGTTGTTGC AGATACGTTG 4413  
(CAP-galO) ATTTA TTCCATGTCA CACTTTCGC A

4414 TAAGTGAAT ATTTATACAC AAAACTACTT TGAAATTAGA CCTCCTGCTG GATCTTGT 4473  
TTACAC A (AP-1)

4474 TTAACATATT AATAAAACAT GTTAAAATT TTGATATTTT GATAATCATA TTTCATTATC 4533  
GAT GTTAAAAT (PRL-FPII)

4534 ATTTGTTCC TTTGTAATCT ATATTTATA TATTTGAAAA CATCTTCTG AGAAGAGTTC 4593  
(GRE-MuRFV) TGTTTTCTG AGAACATCAG

4594 CCCAGATTC ACCAATGAGG TTCTTGGCAT GCACACACAC AGAGTAAGAA CTGATTAGA 4653  
CCAGATCTC ACCATCATTAT (nGRE) CACACACAC A (CACA)  
CTCTGG GGACAC AGAGTAGGG (AP.1-TGFb)

4654 GGCTAACATT GACATTGGTG CCTGAGATGC AAGACTGAAA TTAGAAAGTT CTCCCAAAGA 4713  
(GC2) GATGCT GATGGATAAT TTAGAAGCTT CTCCCACA

4714 TACACAGTTG TTTTAAAGCT AGGGGTGAGG GGGGAAATCT GCCGCTCTA TAGGAATGCT 4773  
(PEA.3)AGGAA GGT

4774 CTCCCTGGAG CCTGGTAGGG TGCTGTCTT GTGTTCTGGC TGGCTGTTAT TTTCTCTGT 4833  
CTC (SSRE) MIR Repeat Region

4834 CCCTGCTACG TCTTAAAGGA CTTGTGGAA TCTCCAGTTC CTAGCATAGT GCCTGGCACA 4893  
GGA CTTGTTGTT CT (GRE-rTAT-II) TGGGCACA  
GCAAAAGGA TCTATTTGGA A (GRE-MMTV)

4894 GTGCAGGTTTC TCAATGAGTT TGCGAGGTGA ATGGAAATAT AAACTAGAAA TATATCCTG 4953  
GTGCCAA (NF-1) (HNF-1)C TGTGAAATAT TAACTAAA

4954 TTGAAATCAG CACACCAGTA GTCTGGTGT AAGTGTGTGT ACGTGTGTGT GTGTGTGT 5013

FIG.1D

APPROVED	O.G. FIG.	
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5014 GTGTGTGT AAAACCAGGT GGAGATATAG GAACTATTAT TGGGGTATGG GTGCATAAAT 5073  
cat/reverse cat box

5074 TGGGATGTTC TTTTAAAAA GAAACTCAA ACAGACTTCT GGAAGGTTAT TTTCTAAGAA 5133  
(1/2GRE)TGTTC T (HSTF) GAAACTTCT GGAATATTCC CGAACTTTC  
C CTTTAGAAA GGA---CAA ACAGAATG(nGRE-Pr1)

5134 TCTTGCTGGC AGCGTGAAGG CAACCCCCCT GTGCACAGCC CCACCCAGCC TCACGTGCC 5193  
(1/2 TRE)AGG CAA T-CC CCAGGCTCCC -CAG(AP.2-SV40)  
GGAGAGCC CC (NF-KB)

5194 ACCTCTGTCT TCCCCATGA AGGGCTGGCT CCCCAGTATA TATAAACCTC TCTGGAGCTC 5253  
tata box GGTC TC (SSRE)

5254 GGGCATGAGC CAGCAAGGC\*C\* ACCCATCCAG GCACCTCTCA GCACAGC 5300  
Start Sites

FIG.1E

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	CLASS      SUBCLASS

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ATC TTTGTTCA GT TTACCTCAGG GCTATTATGA 33

34 AATGAAATGA GATAACCAAT GTGAAAGTCC TATAAACTGT ATAGCCTCCA TTGGATGTA 93  
 94 TGTCTTGGC AGGATGATAA AGAACAGGA AGAAGGAGTA TCCACGTTAG CCAAGTGTCC 153  
 154 AGGCTGTGTC TGCTCTTATT TTAGTGACAG ATGTTGCTCC TGACAGAAGC TATTCTTCAG 213  
 214 GAAACATCAC ATCCAATATG GTAAATCCAT CAAACAGGAG CTAAGAAACA GGAATGAGAT 273  
 274 GGGCACTTGC CCAAGGAAAA ATGCCAGGAG AGCAAATAAT GATGAAAAAT AAACTTTCC 333  
 334 CTTTGTTTT AATTCAGGA AAAAATGATG AGGACCAAAA TCAATGAATA AGGAAAACAG 393  
 394 CTCAGAAAAA AGATGTTCC AAATTGGTAA TTAAGTATTT GTTCCCTGGG AAGAGACCTC 453  
 454 CATGTGAGCT TGATGGAAA ATGGGAAAA CGTCAAAAGC ATGATCTGAT CAGATCCAA 513  
 514 AGTGGATTAT TATTTAAAA ACCAGATGGC ATCACTCTGG GGAGGCAAGT TCAGGAAGGT 573  
 574 CATGTTAGCA AAGGACATAA CAATAACAGC AAAATCAAAA TTCCGCAAAT GCAGGAGGAA 633  
 634 AATGGGGACT GGGAAAGCTT TCATAACAGT GATTAGGCAG TTGACCATGT TCGAACACC 693  
 694 TCCCCGTCTA TACCAGGGAA CACAAAATT GACTGGCTA AGCCTGGACT TTCAAGGGAA 753  
 754 ATATGAAAAA CTGAGAGCAA AACAAAAGAC ATGGTTAAA GGCAACCAGA ACATTGTGAG 813  
 814 CCTTCAAAGC AGCAGTGCCC CTCAGCAGGG ACCCTGAGGC ATTTGCCTTT AGGAAGGCCA 873  
 874 GTTTCTTAA GGAATCTTAA GAAACTCTTG AAAGATCATG AATTTAACCC ATTTTAAGTA 933  
 934 TAAAACAAAT ATGCGATGCA TAATCAGTTT AGACATGGGT CCCAATTTA TAAAGTCAGG 993  
 994 CATAACAAGGA TAACGTGTCC CAGCTCCGGA TAGGTAGAA ATCATTAGAA ATCACTGTGT 1053  
 1054 CCCCATCCTA ACTTTTCAG AATGATCTGT CATAGCCCTC ACACACAGGC CCGATGTGTC 1113  
 1114 TGACCTACAA CCACATCTAC AACCCAAAGTG CCTCAACCCT TGTTAACGTG TCATCTCAGT 1173  
 1174 AGGTCCCATT ACAAAATGCCA CCTCCCCGTG GCAGCCCATC CCCCTCCACA GGAAGTCTCC 1233  
 1234 CCACTCTAGA CTTCTGCATC ACGATGTTAC AGCCAGAAGC TCCGTGAGGG TGAGGGTCTG 1293  
 1294 TGTCTTACAC CTACCTGTAT GCTCTACACC TGAGCTCACT GCAACCTCTG CCTCCCAGGT 1353  
 1354 TCAAGCAATT CTCCTGTCTC AGCCTCCCGC GTAGCTGGGA CTACAGGCGC ACGCCCGGCT 1413  
 1414 AATTTTGTA TTGTTAGTAG AGATGGGGTT TCACCATATT AGCCCGGCTG GTCTTGAAC 1473

FIG.2A

APPROVED	O.G. FIG.	
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1474 CCTGACCTCA GGTGATCCAC CCACCTCAGC CTCCTAAAGT GCTGGGATTA CAGGCATGAG 1533  
 1534 TCACCGCGCC CGGCCAAGGG TCAGTGTAA ATAAGGAATA ACTTGAATGG TTTACTAAAC 1593  
 1594 CAACAGGGAA ACAGACAAAA GCTGTGATAA TTTCAGGGAT TCTTGGGATG GGGAATGGTG 1653  
 1654 CCATGAGCTG CCTGCCTAGT CCCAGACCAC TGGTCCTCAT CACTTCTTC CCTCATCCTC 1713  
 1714 ATTTTCAGGC TAAGTTACCA TTTTATTACAT CATGCTTTG TGGTAAGCCT CCACATCGTT 1773  
 1774 ACTGAAATAA GAGTATAACAT AACTAGTTC CATTGGGGC CATCTGTGTG TGTGTATAGG 1833  
 1834 GGAGGAGGGC ATACCCCAGA GACTCCTGA AGCCCCGGC AGAGGTTTC TCTCCAGCTG 1893  
 1894 GGGGAGCCCT GCAAGCACCC GGGGTCTGG GTGTCTGAG CAACCTGCCA GCCCGTGCCA 1953  
 1954 CTGGTTGTT TGTTATCACT CTCTAGGGAC CTGTTGCTTT CTATTTCTGT GTGACTCGTT 2013  
 2014 CATTCACTCCA GGCATTCATT GACAATTAT TGAGTACTTA TATCTGCCAG ACACCAGAGA 2073  
 2074 CAAAATGGTG AGCAAAGCAG TCACTGCCCT ACCTTCGTGG AGGTGACAGT TTCTCATGGA 2133  
 2134 AGACGTGCAG AAGAAAATTA ATAGCCAGCC AACTTAAACC CAGTGCTGAA AGAAAGGAAA 2193  
 2194 TAAACACCAT CTTGAAGAAT TGTGCGCAGC ATCCCTTAAC AAGGCCACCT CCCTAGCGCC 2253  
 2254 CCCTGCTGCC TCCATCGTGC CGGGAGGCC CCAAGCCGA GTCTTCCAAG CCTCCTCCTC 2313  
 2314 CATCAGTCAC AGCGCTGCAG CTGGCCTGCC TCGCTTCCCG TGAATCGTCC TGGTGCATCT 2373  
 2374 GAGCTGGAGA CTCCTGGCT CCAGGCTCCA GAAAGGAAAT GGAGAGGGAA ACTAGTCTAA 2433  
 2434 CGGAGAATCT GGAGGGGACA GTGTTCTC AGAGGGAAAG GGGCCTCCAC GTCCAGGAGA 2493  
 2494 ATTCCAGGAG GTGGGGACTG CAGGGAGTGG GGACGCTGGG GCTGAGCGGG TGCTGAAAGG 2553  
 2554 CAGGAAGGTG AAAAGGGCAA GGCTGAAGCT GCCCAGATGT TCAGTGTGTT GTACGGGGCT 2613  
 2614 GGGAGTTTC CGTTGCTTCC TGTGAGCCTT TTTATCTTT CTCTGCTTGG AGGAGAAGAA 2673  
 2674 GTCTATTTCA TGAAGGGATG CAGTTTCATA AAGTCAGCTG TAAATTCC AGGGTGTGCA 2733  
 2734 TGGGTTTCC TTCACGAAGG CCTTATTTA ATGGGAATAT AGGAAGCGAG CTCATTTCT 2793  
 2794 AGGCCGTTAA TTCACGGAAG AAGTGAATGG AGTCTTTCT TTCATGTCTT CTGGGCAACT 2853  
 2854 ACTCAGCCCT GTGGTGGACT TGGCTTATGC AAGACGGTCG AAAACCTGG AATCAGGAGA 2913  
 2914 CTCGGTTTC TTTCTGGTTC TGCCATTGGT TGGCTGTGCG ACCGTGGGCA AGTGTCTCTC 2973  
 2974 CTTCCCTGGG CCATAGTCTT CTCTGCTATA AAGACCCCTG CAGCTCTCGT GTTCTGTGAA 3033  
 3034 CACTCCCTG TGATTCTCTG TGAGGGGGGA TGTTGAGAGG GGAAGGAGGC AGAGCTGGAG 3093

FIG.2B

APPROVED	O.G. FIG.	
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3094 CAGCTGAGCC ACAGGGGAGG TGGAGGGGGA CAGGAAGGCA GGCAGAAGCT GGGTGCTCCA 3153  
 3154 TCAGTCCTCA CTGATCACGT CAGACTCCAG GACCGAGAGC CACAATGCTT CAGGAAAGCT 2943  
 2944 CAATGAACCC AACAGCCCACA TTTTCCTTCC CTAAGCATAG ACAATGGCAT TTGCCAATAA 3273  
 3274 CCAAAAAGAA TGCAGAGACT AACTGGTGGT AGCTTTGCC TGGCATTCAA AAACCTGGCC 3333  
 3334 AGAGCAAGTG GAAAATGCCA GAGATTGTTA AACTTTCAC CCTGACCAGC ACCCCACGCA 3393  
 3394 GCTCAGCAGT GACTGCTGAC AGCACGGAGT GACCTGCAGC GCAGGGGAGG AGAAGAAAAA 3453  
 3454 GAGAGGGATA GTGTATGAGC AAGAAAGACA GATTCAATTCA AGGGCAGTGG GAATTGACCA 3513  
 3514 CAGGGATTAT AGTCCACGTG ATCCTGGGTT CTAGGAGGCA GGGCTATATT GTGGGGGGAA 3573  
 3574 AAAATCAGTT CAAGGGAAGT CGGGAGACCT GATTCTAAT ACTATATTTT TCCTTACAA 3633  
 3634 GCTGAGTAAT TCTGAGCAAG TCACAAGGTA GTAACTGAGG CTGTAAGATT ACTTAGTTTC 3693  
 3694 TCCTTATTAG GAACTCTTTT TCTCTGTGGA GTTAGCAGCA CAAGGGCAAT CCCGTTCTT 3753  
 3754 TTAACAGGAA GAAAACATTG CTAAGAGTAA AGCCAAACAG ATTCAAGCCT AGGTCTTGCT 3813  
 3814 GACTATATGA TTGGTTTTTT GAAAATCAT TTCAGCGATG TTTACTATCT GATTGAGAAA 3873  
 3874 ATGAGACTAG TACCCCTTGG TCAGCTGTA ACAAACACCC ATTTGTAAT GTCTCAAGTT 3933  
 3934 CAGGCTTAAC TGCAAGACCA ATCAAATAAG AATAGAATCT TTAGAGCAAA CTGTGTTCT 3993  
 3994 CCACTCTGGA GGTGAGTCTG CCAGGGCAGT TTGGAAATAT TTACTTCACA AGTATTGACA 4053  
 4054 CTGTTGTTGG TATTAACAAC ATAAAGTTGC TCAAAGGCAA TCATTATTTC AAGTGGCTTA 4113  
 4114 AAGTTACTTC TGACAGTTTT GGTATATTAA TTGGCTATTG CCATTTGCTT TTTGTTTTTT 4173  
 4174 CTCTTGGGT TTATTAATGT AAAGCAGGGA TTATTAACCT ACAGTCCAGA AAGCCTGTGA 4233  
 4234 ATTTGAATGA GGAAAAAATT ACGTTTTAT TTTTACCAACC TTCTAACTAA ATTTAACATT 4293  
 4294 TTATTCCATT GCGAATAGAG CCATAAACTC AAAGTGGTAA TAAGAGTACC TGTGATTTG 4353  
 4354 TCATTACCAA TAGAAATCAC AGACATTTA TACTATATTA CAGTTGTTGC AGGTACGTTG 4413  
 4414 TAAGTGAAT ATTTATACTC AAAACTACTT TGAAATTAGA CCTCCTGCTG GATCTGTTT 4473  
 4474 TTAACATATT AATAAAACAT GTTTAAAATT TTGATATTTT GATAATCATA TTTCATTATC 4533  
 4534 ATTTGTTTCC TTTGTAATCT ATATTTATA TATTGAAAA CATCTTCTG AGAAGAGTTC 4593  
 4594 CCCAGATTTC ACCAATGAGG TTCTTGGCAT GCACACACAC AGAGTAAGAA CTGATTAGA 4653  
 4654 GGCTAACATT GACATTGGTG CCTGAGATGC AAGACTGAAA TTAGAAAGTT CTCCCAAAGA 4713

FIG.2C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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4714 TACACAGTTG TTTTAAAGCT AGGGGTGAGG GGGGAAATCT GCCGCTTCTA TAGGAATGCT 4773  
 4774 CTCCCTGGAG CCTGGTAGGG TGCTGTCTT GTGTTCTGGC TGGCTGTTAT TTTCTCTGT 4833  
 4834 CCCTGCTACG TCTTAAAGGA CTTGTTGGA TCTCCAGTTC CTAGCATAGT GCCTGGCACA 4893  
 4894 GTGCAGGTTTC TCAATGAGTT TGCAAGAGTGA ATGGAAATAT AACTAGAAA TATATCTTG 4953  
 4954 TTGAAATCAG CACACCAGTA GTCCTGGTGT AAGTGTGTGT ACGTGTGTGTGTGT GTGTGTGT5017  
 5018 GTGTGTGTGT AAAACCAGGT GGAGATATAG GAACTATTAT TGGGGTATGG GTGCATAAAT 5077  
 5078 TGGGATGTTTC TTTTAAAAAA GAAACTCCAA ACAGACTTCT GGAAGGTTAT TTTCTAAGAA 5137  
 5138 TCTTGCTGGC AGCGTGAAGG CAACCCCCCT GTGCACAGCC CCACCCAGCC TCACGTGGCC 5197  
 5198 ACCTCTGTCT TCCCCCATGA AGGGCTGGCT CCCCAGTATA TATAAACCTC TCTGGAGCTC 5257  
 5258 GGGCATGAGC CAGCAAGGCC ACCCATCCAG GCACCTCTCA GCACAGC 5304

FIG.2D

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APPROVED	O.G. FIG.	
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1 ATCTTGTTCACTTC AGGGCTATTAGAAATGAAA TGAGATAACC  
 51 AATGTGAAAG TCCTATAAAC TGTATAGCCT CCATTCGGAT GTATGTCTT  
 101 GGCAGGATGA TAAAGAATCA GGAAGAAGGA GTATCCACGT TAGCCAAGTG  
 151 TCCAGGCTGT GTCTGCTCTT ATTTAGTGA CAGATGTTGC TCCTGACAGA  
 201 AGCTATTCTT CAGGAAACAT CACATCCAAT ATGGTAAATC CATCAAACAG  
 251 GAGCTAAGAA ACAGGAATGA GATGGGCACT TGCCCAAGGA AAAATGCCAG  
 301 GAGAGCAAAT AATGATGAAA AATAAACTTT TCCCTTGTGTT TTTAATTCA  
 351 GGAAAAAAATG ATGAGGACCA AAATCAATGA ATAAGGAAAA CAGCTCAGAA  
 401 AAAAGATGTT TCCAAATTGG TAATTAAGTA TTTGTTCCCTT GGGAAAGAGAC  
 451 CTCCATGTGA GCTTGATGGG AAAATGGGAA AAACGTCAAAGCAGATGATCT  
 501 GATCAGATCC CAAAGTGGAT TATTATTTA AAAACCAGAT GGCATCACTC  
 551 TGGGGAGGCA AGTCAGGAA GGTCAATGTTA GCAAAGGACA TAACAATAAC  
 601 AGCAAAATCA AAATTCCGCA AATGCAGGAG GAAAATGGGG ACTGGGAAAG  
 651 CTTTCATAAAC AGTGATTAGG CAGTTGACCA TGTTGCAAC ACCTCCCCGT  
 701 CTATACCAGG GAACACAAAA ATTGACTGGG CTAAGCCTGG ACTTTCAAGG  
 751 GAAATATGAA AACTGAGAG CAAAACAAAA GACATGGTTA AAAGGCAACC  
 801 AGAACATTGT GAGCCTCAA AGCAGCAGTG CCCCTCAGCA GGGACCCTGA  
 851 GGCATTTGCC TTTAGGAAGG CCAGTTTCT TAAGGAATCT TAAGAAACTC  
 901 TTGAAAGATC ATGAATTAA ACCATTTAA GTATAAAACA AATATGCGAT  
 951 GCATAATCAG TTTAGACATG GGTCCAATT TTATAAAGTC AGGCATACAA  
 1001 GGATAACGTG TCCCAGCTCC GGATAGGTCA GAAATCATTA GAAATCACTG  
 1051 TGTCCCCATC CTAACCTTTT CAGAATGATC TGTCATAGCC CTCACACACA  
 1101 GGCCCGATGT GTCTGACCTA CAACCACATC TACAACCCAA GTGCCTCAAC  
 1151 CATTGTTAAC GTGTCATCTC AGTAGGTCCC ATTACAAATG CCACCTCCCC  
 1201 TGTGCAGCCC ATCCCGCTCC ACAGGAAGTC TCCCCACTCT AGACTTCTGC  
 1251 ATCACGATGT TACAGCCAGA AGCTCCGTGA GGGTGAGGGT CTGTTCTTA

FIG.3A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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1301 CACCTACCTG TATGCTCTAC ACCTGAGCTC ACTGCAACCT CTGCCCTCCA  
 1351 GGTTCAAGCA ATTCTCCTGT CTCAGCCTCC CGCGTAGCTG GGACTACAGG  
 1401 CGCACGCCCG GCTAATTTT GTATTGTTAG TAGAGATGGG GTTTCACCAT  
 1451 ATTAGCCCGG CTGGTCTTGA ACTCCTGACC TCAGGTGATC CACCCACCTC  
 1501 AGCCTCCTAA AGTGCTGGGA TTACAGGCAT GAGTCACCGC GCCCGGCCAA  
 1551 GGGTCAGTGT TTAATAAGGA ATAACTTGAA TGGTTTACTA AACCAACAGG  
 1601 GAAACAGACA AAAGCTGTGA TAATTCAGG GATTCTGGG ATGGGGAATG  
 1651 GTGCCATGAG CTGCCTGCCT AGTCCCAGAC CACTGGTCCT CATCACTTTC  
 1701 TTCCCTCATC CTCATTTCA GGCTAAGTTA CCATTTATT CACCATGCTT  
 1751 TTGTGGTAAG CCTCCACATC GTTACTGAAA TAAGAGTATA CATAAACTAG  
 1801 TTCCATTTGG GGCCATCTGT GTGTGTGTAT AGGGGAGGGAG GGCATACCCC  
 1851 AGAGACTCCT TGAAGCCCCC GGCAGAGGTT TCCTCTCCAG CTGGGGGAGC  
 1901 CCTGCAAGCA CCCGGGGTCC TGGGTGTCTT GAGCAACCTG CCAGCCGTG  
 1951 CCACTGGTTG TTTTGTATC ACTCTCTAGG GACCTGTTGC TTTCTATTTC  
 2001 TGTGTGACTC GTTCATTATC CCAGGCATTC ATTGACAATT TATTGAGTAC  
 2051 TTATATCTGC CAGACACCAG AGACAAAATG GTGAGCAAAG CAGTCACTGC  
 2101 CCTACCTTCG TGGAGGTGAC AGTTTCTCAT GGAAGACGTG CAGAAGAAAA  
 2151 TTAATAGCCA GCCAACTTAA ACCCAGTGCT GAAAGAAAGG AAATAAACAC  
 2201 CATCTTGAAG AATTGTGCGC AGCATCCCTT ACAAGGCCA CCTCCCTAGC  
 2251 GCCCCCTGCT GCCTCCATCG TGCCCGGAGG CCCCCAAGCC CGAGTCTTCC  
 2301 AAGCCTCCTC CTCCATCAGT CACAGCGCTG CAGCTGGCCT GCCTCGCTTC  
 2351 CCGTGAATCG TCCTGGTGCA TCTGAGCTGG AGACTCCTG GCTCCAGGCT  
 2401 CCAGAAAGGA AATGGAGAGG GAAACTAGTC TAACGGAGAA TCTGGAGGGG  
 2451 ACAGTGTTC CTCAGAGGGA AAGGGGCCTC CACGTCCAGG AGAATTCCAG  
 2501 GAGGTGGGGA CTGCAGGGAG TGGGGACGCT GGGGCTGAGC GGGTGCTGAA  
 2551 AGGCAGGAAG GTGAAAAGGG CAAGGCTGAA GCTGCCAGA TGTTCAAGTGT  
 2601 TGTTCACGGG GCTGGGAGTT TTCCGTTGCT TCCTGTGAGC CTTTTATCT

FIG.3B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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2651 TTTCTCTGCT TGGAGGGAGAA GAAGTCTATT TCATGAAGGG ATGCAGTTTC  
 2701 ATAAAGTCAG CTGTTAAAAT TCCAGGGTGT GCATGGGTTT TCCTTCACGA  
 2751 AGGCCTTTAT TTAATGGAA TATAGGAAGC GAGCTCATT CCTAGGCCGT  
 2801 TAATTACCGG AAGAAGTGAC TGGAGTCTTT TCTTCATGT CTTCTGGGCA  
 2851 ACTACTCAGC CCTGTGGTGG ACTTGGCTTA TGCAAGACGG TCGAAAACCT  
 2901 TGGAATCAGG AGACTCGGTT TTCTTCTGG TTCTGCCATT GGTTGGCTGT  
 2951 GCGACCGTGG GCAAGTGTCT CTCCTCCCT GGGCCATAGT CTTCTCTGCT  
 3001 ATAAAGACCC TTGCAGCTCT CGTGTCTGT GAACACTTCC CTGTGATTCT  
 3051 CTGTGAGGGGG GGATGTTGAG AGGGGAAGGA GGCAGAGCTG GAGCAGCTGA  
 3101 GCCACAGGGGG AGGTGGAGGG GGACAGGAAG GCAGGCAGAA GCTGGGTGCT  
 3151 CCATCAGTCC TCACTGATCA CGTCAGACTC CAGGACCGAG AGCCACAATG  
 3201 CTTCAGGAAA GCTCAATGAA CCCAACAGCC ACATTTCTT TCCCTAAGCA  
 3251 TAGACAATGG CATTGCCAA TAACCAAAAA GAATGCAGAG ACTAACTGGT  
 3301 GGTAGCTTTT GCCTGGCATT CAAAAACTGG GCCAGAGCAA GTGGAAAATG  
 3351 CCAGAGATTG TTAAACTTTT CACCCCTGACC AGCACCCAC GCAGCTCAGC  
 3401 AGTGAUTGCT GACAGCACGG AGTGAUTGC AGCGCAGGGG AGGAGAAGAA  
 3451 AAAGAGAGGG ATAGTGTATG AGCAAGAAAG ACAGATTCA TCAAGGGCAG  
 3501 TGGGAATTGA CCACAGGGAT TATAGTCCAC GTGATCCTGG GTTCTAGGAG  
 3551 GCAGGGCTAT ATTGTGGGGG GAAAAAAATCA GTTCAAGGGAA AGTCGGGAGA  
 3601 CCTGATTCT AATACTATAT TTTTCTTAA CAAGCTGAGT AATTCTGAGC  
 3651 AAGTCACAAG GTAGTAUTG AGGCTGTAAG ATTACTTAGT TTCTCCTTAT  
 3701 TAGGAUTCT TTTTCTCTGT GGAGTTAGCA GCACAAGGGC AATCCGTTT  
 3751 CTTTAACAG GAAGAAAACA TTCCTAAGAG TAAAGCCAAA CAGATTCAAG  
 3801 CCTAGGTCTT GCTGAUTATA TGATTGGTTT TTTGAAAAAT CATTTCAGCG  
 3851 ATGTTTACTA TCTGATTCAAG AAAATGAGAC TAGTACCCCTT TGGTCAGCTG  
 3901 TAAACAAACA CCCATTGTA AATGTCTCAA GTTCAGGCTT AACTGCAGAA  
 3951 CCAATCAAAT AAGAATAGAA TCTTAGAGC AACTGTGTT TCTCCACTCT

FIG.3C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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4001 GGAGGTGAGT CTGCCAGGGC AGTTTGGAAA TATTTACTTC ACAAGTATTG  
 4051 ACACTGTTGT TGGTATTAAC AACATAAAGT TGCTCAAAGG CAATCATTAT  
 4101 TTCAAGTGGC TTAAAGTTAC TTCTGACAGT TTTGGTATAT TTATTGGCTA  
 4151 TTGCCATTG CTTTTGTTT TTTCTTTG GGTTTATTAA TGAAAGCAG  
 4201 GGATTATTAA CCTACAGTCC AGAAAGCCTG TGAATTGAA TGAGGAAAAA  
 4251 ATTACATTAA TGTTTTTACCC ACCTTCTAAC TAAATTAAAC ATTTTATTCC  
 4301 ATTGCGAATA GAGCCATAAA CTCAAAGTGG TAATAACAGT ACCTGTGATT  
 4351 TTGTCATTAC CAATAGAAAT CACAGACATT TTATACTATA TTACAGTTGT  
 4401 TGCAGATACG TTGTAAGTGA AATATTATA CTCAAAACCA CTTGAAATT  
 4451 AGACCTCCTG CTGGATCTTG TTTTAACAT ATTAATAAAA CATGTTAAA  
 4501 ATTTGATAT TTTGATAATC ATATTCATT ATCATTGTT TCCTTGAA  
 4551 TCTATATTAA ATATATTGA AAACATCTT CTGAGAAGAG TTCCCCAGAT  
 4601 TTCACCAATG AGGTTCTGG CATGCACACA CACAGAGTAA GAACTGATT  
 4651 AGAGGCTAAC ATTGACATTG GTGCCTGAGA TGCAAGACTG AAATTAGAAA  
 4701 GTTCTCCCAA AGATACACAG TTGTTTAAA GCTAGGGGTG AGGGGGGAAA  
 4751 TCTGCCGCTT CTATAGGAAT GCTCTCCCTG GAGCCTGGTA GGGTGCTGTC  
 4801 CTTGTGTTCT GGCTGGCTGT TATTTTCTC TGTCCTGCT ACGTCTAAA  
 4851 GGACTTGTAA GGATCTCCAG TTCCCTAGCAT AGTGCCTGGC ACAGTGCAGG  
 4901 TTCTCAATGA GTTGCAGAG TGAATGGAAA TATAAACTAG AAATATATCC  
 4951 TTGTTGAAAT CAGCACACCA GTAGTCCTGG TGTAAGTGTG TGTACGTGTG  
 5001 TGTGTGTGTG TGTGTGTGTG TGTAAAACCA GGTGGAGATA TAGGAACTAT  
 5051 TATTGGGGTA TGGGTGCATA AATTGGGATG TTCTTTTAA AAAGAAACTC  
 5101 CAAACAGACT TCTGGAAGGT TATTTCTAA GAATCTTGCT GGCAGCGTGA  
 5151 AGGCAACCCC CCTGTGCACA GCCCCACCCA GCCTCACGTG GCCACCTCTG  
 5201 TCTTCCCCCA TGAAGGGCTG GCTCCCCAGT ATATATAAAC CTCTCTGGAG  
 5251 CTCGGGCATG AGCCAGCAAG GCCACCCATC CAGGCACCTC TCAGCACAGC 5300

**FIG.3D**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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1 AGAGCTTCCAGAGGAAGCCTACCAAGCCTGCAATGAGGTTCTCTGTGCACGTTGC 60  
61 TGCAGCTTGGCCTGAGATGCCAGCTGTCCAGCTGCTGCTTCTGGCCTGCCTGGTGTGG 120  
121 GATGTGGGGGCCAGGACAGCTCAGCTCAGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180  
181 TATACCTTCAGTGTGGCCAGTCCCATGAATCCAGCTGCCAGAGCAGAGCCAGGCCATG 240  
241 TCAGTCATCCATAACTTACAGAGAGACAGCAGCACCCAACGCTTAGACCTGGAGGCCACC 300  
301 AAAGCTGACTCAGCTCCCTGGAGAGGCCTCTCCACCAATTGACCTGGACCAGGCTGCC 360  
361 AGGCCCCAGGAGACCCAGGAGGGGCTGCAGAGGGAGCTGGGCACCCCTGAGGCGGGAGCGG 420  
421 GACCAGCTGAAACCCAAACCAGAGAGTTGGAGACTGCCTACAGCAACCTCCGAGAC 480  
481 AAGTCAGTTCTGGAGGAAGAGAAGAAGCGACTAAGGCAAGAAAATGAGAATCTGGCCAGG 540  
541 AGGTTGGAAAGCAGCAGCCAGGAGGTAGCAAGGCTGAGAAGGGCCAGTGTCCCCAGACC 600  
601 CGAGACACTGCTCGGGCTGTGCCACCAGGCTCCAGAGAAG

(exon #2) TT TCT ACG TGG AAT TTG GAC

661 ACT TTG GCC TTC CAG GAA CTG AAG TCC GAG CTA ACT GAAG TT CCT GCT TCC CGA ATT TTG 720  
721 AAG GAG AGC CCA TCT GGC TAT CTC AGG AGT GGA GAG GGA GAC ACCG

(intron #2)  
gtatgaagttaagttcttccctttgtccccacgtggctttattcatgtctagtgctgtgttcagagaa  
tcagtataggtaaatgcccacccaaagggggaaattaactccctggagcagagggagggagggagga  
gaagaggaacagaactctctctctctgttacccttgt-----Intron II - 3 kb-----

FIG. 3E

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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tggctctgccaaggcttccgcatgatcatgttggaaagattatggattaaagtggcttcgtttt  
cttctgaatttaccag

(exon #3) GA TGT GGA GAA CTA 780

781 GTT TGG GTA GGA GAG CCT CTC ACG CTG AGA ACA GCA GAA ACA ATT ACT GGC AAG TAT GGT 840  
841 GTG TGG ATG CGA GAC CCC AAG CCC ACC TAC CCC TAC ACC CAG GAG ACC ACG TGG AGA ATC 900  
901 GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC AGC CAG TTT ATG 960  
961 CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CTC AGG CCA CTG GAA AGC ACG GGT GCT GTG 1020  
1021 GTG TAC TCG GGG AGC CTC TAT TTC CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG 1080  
1081 CTG AAT ACC GAG ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG 1140  
1141 TTC CCG TAT TCT TGG GGT GGC TAC AGC GAC ATT GAC TTG GCT GTG GAT GAA GCA GGC CTC 1200  
1201 TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC ATT GTC CTC AAA CTG AAC CCA 1260  
1261 GAG AAT CTG GAA CTC GAA CAA ACC TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT 1320  
1321 GCC TTC ATC ATC TGT GGC ACC TTG TAC ACC GTC AGC TAC ACC TCA GCA GAT GCT ACC 1380  
1381 GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC CCA TTC AAG 1440  
1441 AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC CCC CTG GAG AAG CTC TCC AAG ATG 1500  
1501 TGG GAC AAC TTG AAC ATG GTC ACT TAT GAC ATC AAG CTC TCC TCC AAG ATG

(3' flanking region) TGA AAA GCC TCC TCC 1560  
1561 AAG CTG TAC AGG CAA TGG CAG AAG GAG ATG CTC AGG GCT CCT GGG GGG AGC AGG CTG AAG 1620  
1621 GGA GAG CCA GCC AGC CAG GGC CCA GGC AGC ATG TAA CTC TAA CTA TCC AGG AAT TGT AGT TTT CCA AGT 1680  
1681 AGA AGG ATG AAC ATG GTC ACC ATC TAA CTC TAA CTA TCC AGG AAT TGT AGT CTG AGG GCG TAG ACA 1740  
1741 ATT TCA TAT AAT TAA TAT CCT TTA TCT TCT GTC AGC ATT TAT GGG ATG TTT AAT GAC ATA 1800  
1801 GTT CAA GTT TTC TTG TGA TTT GGG GCA AAA GCT GTC AGG CAT AAT AGT CTT TTC CTG AAA 1860  
1861 ACC ATT GCT CTT GCA TGT TAC ATG GTT ACC ACA AGC CAC AAT AAA AAG CAT AAC TTC TAA 1920  
1921 AGG AAG CAG AAT AGC TCC TCT GGC CAG CAT CGA ATA TAA GAA TGC ATT TAC TAC AGT 1980  
1981 TGG CTT CTA ATG CTT CAG ATA GAA TAC AGT TGG GTC TCA CAT AAC CCT TAC ATT GTG AAA 2040  
2041 TAA AAT TTT CTT ACC CAA CGT TCT CCT CCT TGA ACT TTG TGG GAA TCT TTG CTT AAG AGA 2100  
2101 AGG ATA TAG ATT CCA ACC ATC AGG TAA TTC CTT CAG GTT GGG AGA TGT GAT TGC AGG ATG 2160

FIG.3F

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
GAFTSMAH		

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2161 TTA AAG GTG TGT GTG TGT GTG TGT GTG TAA CTG AGA GGC TTG TGC CTG GTT TTG 2220  
2221 AGG TGC TGC CCA GGA TGA CGC CAA GCA AAT AGC GCA TCC ACA CTT TCC CAC CTC CAT CTC 2280  
2281 CTG GTG CTC TCG GCA CTA CCG GAG CAA TCT TTC CAT CTC TCC CCT GAA CCC ACC CTC TAT 2340  
2341 TCA CCC TAA CTC CAC TTC AGT TTG CTT TTG ATT TTT TTT TTT TTT TTT TGA 2400  
2401 GAT GGG GTC TCG CTC TGT CAC CCA GGC TGG AGT GCA GTG GCA CGA TCT CGG CTC ACT GCA 2460  
2461 AGT TCC GCC TCC CAG GTT CAC ACC ATT CTC CTG CCT CAG CCT CCC AAG TAG CTG GGA CTA 2520  
2521 CAG GCA CCT GCC ACC ACG CCT GGC TAA TTT TTT TTT CCA GTG AAG ATG GGT TTC ACC 2580  
2581 ATG TTA GCC AGG ATG GTC TCG ATC TCC TGAC CTT GTC ATC CAC CCA CCT TGG CCT CCC AAA 2640  
2641 GTG CTG GGA TTA CAG GCG TGA GCC ACC ACGC OCA GCC CCT CCA CTT CAG TTT TTA TCT GTC 2700  
2701 ATC AGG GGT ATG AAT TTT ATA AGC CAC ACC TCA GGT GGA GAA AGC TTG ATG CAT AGC TTG 2760

FIG. 3G

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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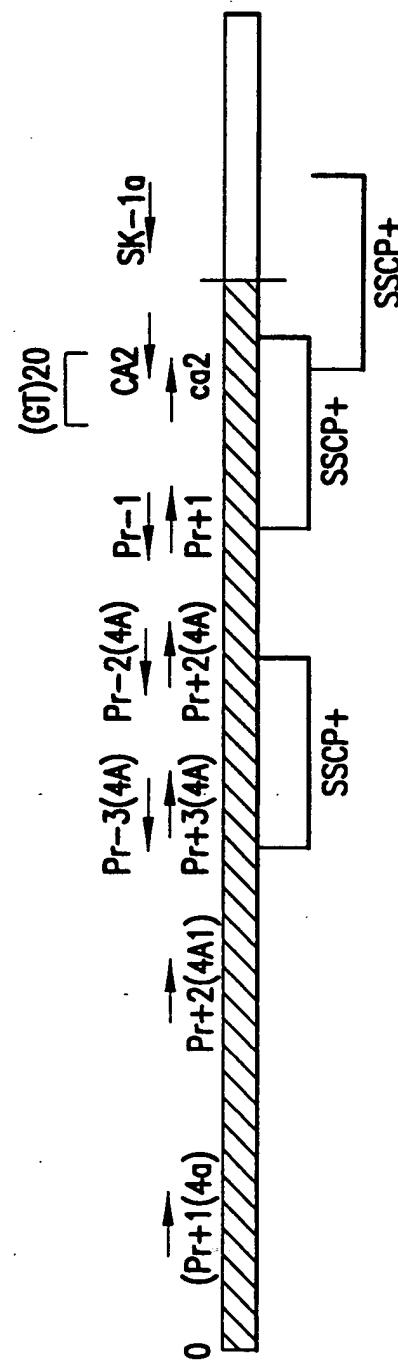


FIG.4

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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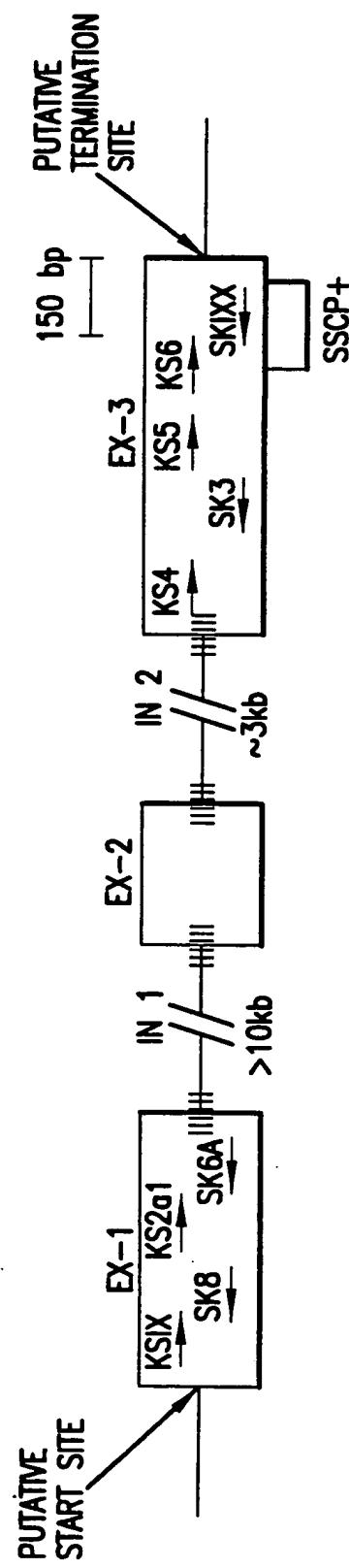


FIG.5

65 P-10 = 138222520

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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TIGR	-TGAVVYSGS	LYFQGAESRT	VIRYELNTET	VKAEEKIIPGA	GYHGQFPYSW	GGYTDIDLAV	59
ym08h12.r1	-----	-----	-----	--RFDLKTT	ILKTRSLDYA	GYNNMYHYAW	38
1B426bAMZ	GTGQVVWYNGS	IYFQNKFQSHI	IIRFDLKTT	ILKTRSLDYA	GYNNMYHYAW	GGHSDIDLW	60
ranofm	GAGVVVWHINNN	LYYNCFNSHD	MCRASL-TSG	YVQKKPLLNA	LFNNRFSYAG	TMFQDMDFSS	59
Consensus	..G..VW....	..Y....S...	..R..L..TET	.....L..A	GYNN...	YAW	GG..DIDL..V

TIGR	DEAGLWIYS	TDEAKGAIVL	SKLNPEENEL	EQTWETNIRK	QSUVANAFIIC	GTLYTVSSYT	119
ym08h12.r1	DESGLWAVYA	TNQNAGNIIV	SRLDPVSLQT	LQTWNTSYPK	RXPGXAFIIC	GTCYVVTNGY-	97
1B426bAMZ	DENGLWAVYA	TNQNAGNIIV	SKLDPVSLQI	LQTWNTSYPK	RSAGEAFIIC	GTLYVVTNGYS	120
ranofm	DEKGLWVIFT	TEKSAGKIVV	GKVNWATFTV	DNIWITTONQK	SDASNAFMIC	GVLVYVTRSLG	119
Consensus	DE..GLW..Y.	T..AG..IV.	SKL..P..L..	..QTW..T..K..	..AFIIC	GTLYVT..Y.	120

TIGR	SADATVNFAY	DTGTGISKTL	TIPFKNRKY	SSMIDYNPLE	KKLFAWDNLN	MVTYDIKLS	178
ym08h12.r1	SGGTKVHYAY	QTNAST-----	-----YEY	-----IDI	-PFQ	NKLXP-----	131
1B426bAMZ	GG-TKVHYAY	QTNASTYEYI	DIPFQNKYSH	ISMLDYNPKD	RALYAWNNGH	-HFP-----	178
ranofm	PKMEEVFYMF	DTKTGKEGHL	SIMMEKMAEK	VHSLSYNSND	RKL YMFSEGY	LLHYDIAL-	177
Consensus	.....V.YAY	.T.....	..I.....Y..	..DYNP..	.KL.....	..Y..L..	178

FIG. 6

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

20/23

1 AGA GCT TTC CAG AGG AAG CCT CAC CAA GCC TCT GCA ATG AGG TTC TTC TGT GCA CGT TGC 60  
 61 TGC AGC TTT GGG CCT GAG ATG CCA GCT GTC CAG CTG CTT CTG GCC CTG CTG GTC TGG TGG 120  
 121 GAT GTG GGG GCC AGG ACA GCT CAG CTC AGG AAG GCC AAT GAC CAG AGT GGC CGA TGC CAG 180  
 181 TAT ACC TTC AGT GTG GCC AGT CCC AAT GAA TCC AGC TGC CCA GAG CAG AGC CAG GCC ATG 240  
 241 TCA GTC ATC CAT AAC TTA CAG AGA GAC AGC AGC ACC CAA CGC TTA GAC CTG GAG GCC ACC 300  
 301 AAA GCT CGA CTC AGC TCC CTG GAG AGC CTC CTC CAC CAA TTG ACC TTG GAC CAG GCT GCC 360  
 361 AGG CCC CAG GAG ACC CAG GAG GGG CTG CAG AGG GAG CTG GGC ACC CTG AGG CGG GAG CGG 420  
 421 GAC CAG CTG GAA ACC CAA ACC AGA GAG TTG GAG ACT GCC TAC AGC AAC CTC CTC CGA GAC 480  
 481 AAG TCA GTT CTG GAG GAA GAG AAG CGA CTA AGG CAA GAA AAT GAG AAT CTG GCC AGG 540  
 541 AGG TTG GAA AGC AGC AGC CAG GAG GCA AGG CTG AGA AGG GGC CAG TGT CCC CAG ACC 600  
 601 CGA GAC ACT GCT CGG GCT GTG CCA CCA GGC TCC AGA GAA GTT TCT ACG TGG AAT TTG GAC 660  
 661 ACT TTG GCC TTC CAG GAA CTG AAG TCC GAG CTA ACT GAA GTT CCT GCT TCC CGA ATT TTG 720  
 721 AAG GAG AGC CCA TCT GGC TAT CTC AGG AGT GGA GAG GGA GAC ACC GGA TGT GGA GAA CTA 780  
 781 GTT TGG GTA GGA GAG CCT CTC ACG CTG AGA ACA GCA GAA ACA ATT ACT GGC AAG TAT GGT 840  
 841 GTG TGG ATG CGA GAC CCC AAG CCC ACC TAC CCC TAC ACC CAG GAG ACC ACG TGG AGA ATC 900

FIG. 7A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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901 GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC AGC CAG TTT ATG 960  
 961 CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CCT AGG CCA CTG GAA AGC ACG GGT GCT GTG 1020  
 1021 GTG TAC TCG GGG AGC CTC TAT TTC CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG 1080  
 1081 CTG AAT ACC GAG ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG 1140  
 1141 TTC CCG TAT TCT TGG GGT GGC TAC ACG GAC ATT GAC TTG GCT GTG GAT GAA GCA GGC CTC 1200  
 1201 TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC ATT GTC CTC TCC AAA CTG AAC CCA 1260  
 1261 GAG AAT CTG GAA CAA ACC TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT 1320  
 1321 GCC TTC ATC ATC TGT GGC ACC TTG TAC ACC GTC AGC AGC TAC ACC TCA GCA GAT GCT ACC 1380  
 1381 GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC ATC CCA TTC AAG 1440  
 1441 AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC CCC CTG GAG AAG CTC TTT GCC 1500  
 1501 TGG GAC AAC TTG AAC ATG GTC ACT TAT GAC ATC AAG CTC TCC AAG ATG 1548

FIG. 7B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

22/23

1 Met Arg Phe Phe Cys Ala Arg Cys 20  
 21 Cys Ser Phe Gly Pro Glu Met Pro Ala Val Gln Leu Leu Leu Ala Cys Leu Val Trp 40  
 41 Asp Val Gly Ala Arg Thr Ala Gln Leu Arg Lys Ala Asn Asp Gln Ser Gly Arg Cys Gln 60  
 61 Tyr Thr Phe Ser Val Ala Ser Pro Asn Glu Ser Ser Cys Pro Glu Gln Ser Gln Ala Met 80  
 81 Ser Val Ile His Asn Leu Gln Arg Asp Ser Ser Thr Gln Arg Leu Asp Leu Glu Ala Thr 100  
 101 Lys Ala Arg Leu Ser Ser Leu Glu Ser Leu Leu His Gln Leu Thr Leu Asp Gln Ala Ala 120  
 121 Arg Pro Gln Glu Thr Gln Glu Gly Leu Gln Arg Glu Leu Gly Thr Leu Arg Arg Glu Arg 140  
 141 Asp Gln Leu Glu Thr Gln Thr Arg Glu Leu Glu Thr Ala Tyr Ser Asn Leu Leu Arg Asp 160  
 161 Lys Ser Val Leu Glu Glu Lys Lys Arg Leu Arg Gln Glu Asn Glu Asn Leu Ala Arg 180  
 181 Arg Leu Glu Ser Ser Ser Gln Glu Val Ala Arg Leu Arg Arg Gly Gln Cys Pro gln Thr 200  
 201 Arg Asp Thr Ala Arg Ala Val Pro Pro Gly Ser Arg Glu Val Ser Thr Trp Asn Leu Asp 220  
 221 Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val Pro Ala Ser Arg Ile Leu 240  
 241 Lys Glu Ser Pro Ser Gly Tyr Leu Arg Ser Gly Glu Gly Asp Thr Gly Cys Gly Glu Leu 260  
 261 Val Trp Val Gly Glu Pro Leu Thr Leu Arg Thr Ala Glu Thr Ile Thr Gly Lys Tyr Gly 280  
 281 Val Trp Met Arg Asp Pro Lys Pro Tyr Thr Tyr Pro Tyr Thr Glu Thr Thr Trp Arg Ile 300

**FIG.8A**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

23/23

301 Asp Thr Val Gly Thr Asp Val Arg Gln Val Phe Glu Tyr Asp Leu Ile Ser Gln Phe Met 320  
 321 Gln Gly Tyr Pro Ser Lys Val His Ile Leu Pro Arg Pro Leu Glu Ser Thr Gly Ala Val 340  
 341 Val Tyr Ser Gly Ser Leu Tyr Phe Gln Gly Ala Glu Ser Arg Thr Val Ile Arg Tyr Glu 360  
 361 Leu Asn Thr Glu Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His Gly Gln 380  
 381 Phe Pro Tyr Ser Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala Val Asp Glu Ala Gly Leu 400  
 401 Trp Val Ile Tyr Ser Thr Asp Glu Ala Lys Gly Ala Ile Val Leu Ser Lys Leu Asn Pro 420  
 421 Glu Asn Leu Glu Leu Glu Gln Thr Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn 440  
 441 Ala Phe Ile Ile Cys Gly Thr Leu Tyr Thr Val Ser Ser Tyr Thr Ser Ala Asp Ala Thr 460  
 461 Val Asn Phe Ala Tyr Asp Thr Gly Thr Ile Ser Lys Thr Leu Thr Ile Pro Phe Lys 480  
 481 Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp Tyr Asn Pro Leu Glu Lys Lys Leu Phe Ala 500  
 501 Trp Asp Asn Leu Asn Met Val Thr Tyr Asp Ile Lys Leu Ser Lys Met

FIG. 8B